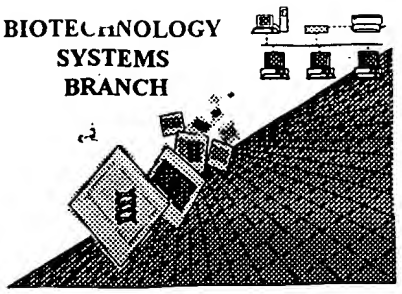

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/805,427

Source: OIPE

Date Processed by STIC: 7/24/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/805,427

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single **nucleotide** in a nucleic acid sequence. N is **not** used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/805,427

DATE: 07/24/2001
TIME: 10:49:10

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\07242001\I805427.raw

Does Not Comply
Corrected Diskette Needed

pp 1-2

```
     4 <110> APPLICANT: Statens Serum Institut
     6 <120> TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
     9 <130> FILE REFERENCE: 20486US03
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/805,427
C--> 11 <141> CURRENT FILING DATE: 2001-03-13
    11 <160> NUMBER OF SEQ ID NOS: 12
    13 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

   273 <210> SEQ ID NO: 12
   274 <211> LENGTH: 20
   275 <212> TYPE: DNA
   276 <213> ORGANISM: Artificial Sequence
W--> 277 <220> FEATURE: oligonucleotide
W--> 277
W--> 279 <223> OTHER INFORMATION:
   279 <400> SEQUENCE: 12
   280  ccttcggtgg atcccgtcag
W--> 285 PATENT
E--> 286 670001-2002.5
E--> 287 1
E--> 290 sequence Listing07/24/01
W--> 291 PLOUGMANN, VINGTOFT & PARTNERS
E--> 293 20486us03/as/07/24/01
```

(Global error)

DO NOT insert a response to <2207. <2207 is a "header" only. Explanation for Artificial Sequence or Unknown goes on 20 <2237 line.

delete

FYI, "oligonucleotide" is an invalid explanation for Artificial Sequence (or Unknown). Give source of genetic material, see Item 11 on Error Summary Sheet. Please correct all sequences showing this error

↓

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

see next page for more errors

<210> 3
<211> 404
<212> PRT
<213> Artificial Sequence
<220> oligonucleotide

another example of global error

<400> 3

Met	Ala	Thr	Val	Asn	Arg	Ser	Arg	His	His	His	His	His	His	His
1				5				10					15	

VERIFICATION SUMMARY DATE: 07/24/2001
PATENT APPLICATION: **US/09/805,427** TIME: 10:49:11

Input Set : **A:\PTO_VSK.txt**
Output Set: **N:\CRF3\07242001\I805427.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:91 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:93 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:151 M:283 W: Missing Blank Line separator, <220> field identifier
L:151 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:153 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:212 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:223 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:225 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:232 M:283 W: Missing Blank Line separator, <220> field identifier
L:232 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:234 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:241 M:283 W: Missing Blank Line separator, <220> field identifier
L:241 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:243 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:250 M:283 W: Missing Blank Line separator, <220> field identifier
L:250 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:252 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:259 M:283 W: Missing Blank Line separator, <220> field identifier
L:259 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:261 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:268 M:283 W: Missing Blank Line separator, <220> field identifier
L:268 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:270 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:277 M:283 W: Missing Blank Line separator, <220> field identifier
L:277 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:279 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:285 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:286 M:254 E: No. of Bases conflict, LENGTH:Input:5 Counted:22 SEQ:12
L:286 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:12
L:287 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:22 SEQ:12
L:290 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:290 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:290 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:39 SEQ:12
L:290 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:13
L:290 M:112 C: (48) String data converted to lower case,
L:291 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:293 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:47 SEQ:12
L:293 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:15
L:293 M:112 C: (48) String data converted to lower case,
L:293 M:252 E: No. of Seq. differs, <211>LENGTH:Input:20 Found:47 SEQ:12